

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 5, line 5 with the following rewritten paragraph:

FigureFIG. 2 shows the cDNA and deduced amino acid sequences of human *PIN1* and homologies with other WW domain proteins and PPIases. FigureFIG. 2A shows the Pin1 nucleotide sequence (SEQ ID NO: 1) and predicted Pin1-amino acid sequence (SEQ ID NO: 2) (isas indicated in one-letter code). The fusion points between GAL4 and Pin1 in six different isolated clones were: clone H20 at C-9; clone H16.24 and 38 at G:13G+13; clones H6 and H36 at C:15C+15. Underlined residues form a consensus bipartite nuclear localization signal. The N- and C-terminal boxes indicate the WW domain and PPIase domain, respectively. Nucleotide numbers are on the left and amino acid numbers on right. FigureFIG. 2B and 2C shows alignmentsthe alignment of the WW domain (B) and PPIase Domain (C) in selected proteins (from top to bottom SEQ ID NOs: 8-14). FIG. 2C shows the alignment of the PPIase domain in selected proteins (from top to bottom SEQ ID NOs: 15-21). In FIGs. 2B and 2C, Identicalidentical residues are shown in the bottom-row labeled “Consensus” (SEQ ID NO: 22). Dashes indicate gaps introduced to make the alignment. Cbf2, cell binding factor 2; SC, *S. cerevisiae*; EC, *E. coli*; BS, *B. subtilis*; CJ, *C. jejuni*; AT, *A. thaliana*.